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A. CTTATCGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT
CACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA
+++++ ↑ ++++++
ATGTATCTTATCATGTC CLEAVAGE SITE

B.  AAUAAA
+++++ GCA

C.  GCAaaaaaaaaaaaaaaaaaaaaa

+ UPSTREAM AND DOWNSTREAM
CLEAVAGE-POLYADENYLATION ELEMENTS

Fig. 1



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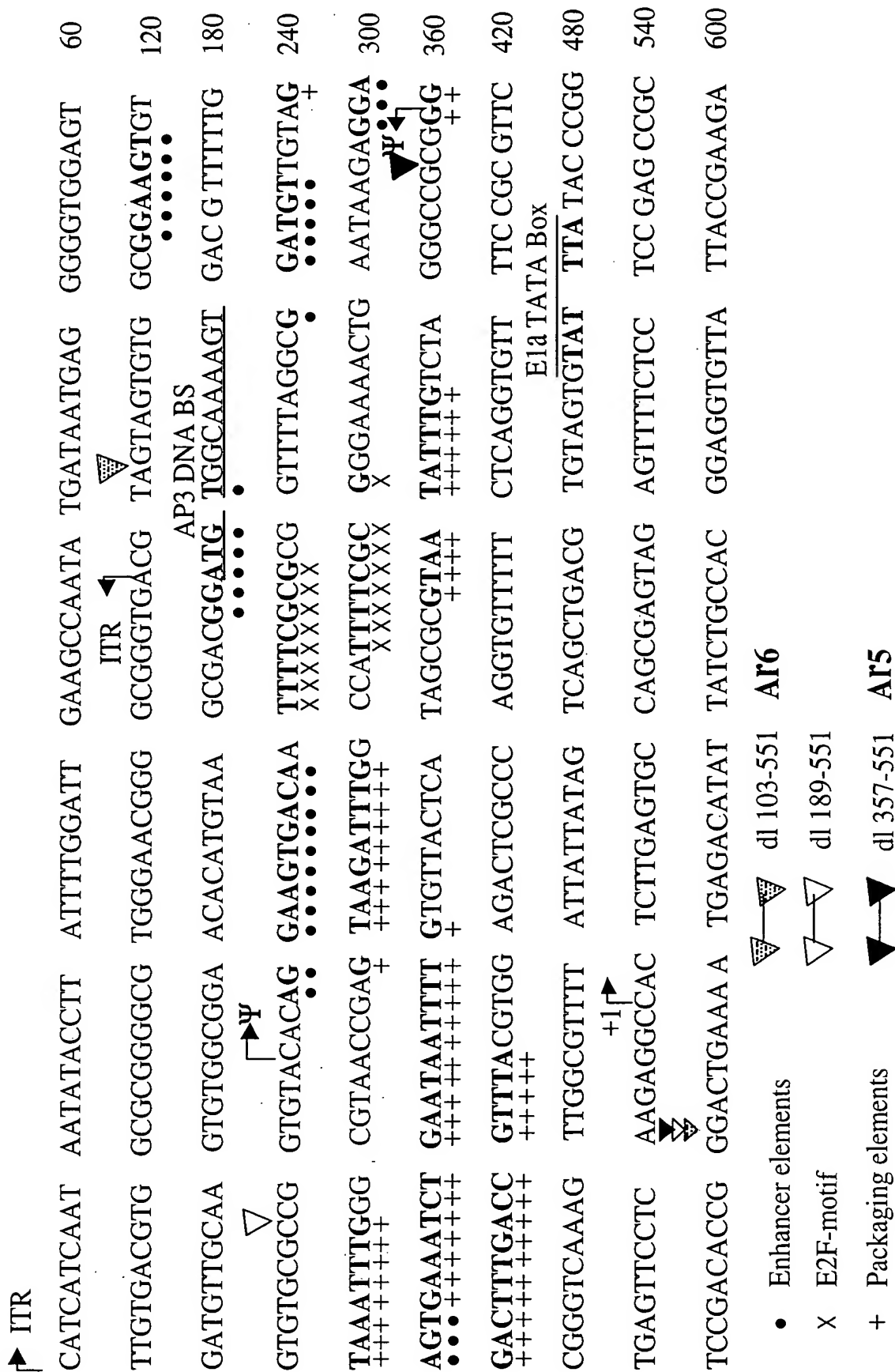


Fig. 2



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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----
61 TTGTGACGTGGCGCGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
+-----ITR-----+ +---
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----
181 ACAAATTTACAAATAAAGCATTTTTTTCAGTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATCATCCGGACAAAGCCTGC
-----+ +-----
301 GCGCGCCCCGCCCCGCCATTGGCCGTACCGCCCCGCGCCGCGCCCCATCTCGCCCCCTCG
-----E2F-1 PROMOTER-----
361 CCGCCGGGTCCGGCGCGTTAAAGCCAATAGGAACCGCCGCGTGTTCCTCCGTCACGGCCG
-----E2F-1 PROMOTER-----
421 GGGCAGCCAATTGTGGCGGCGCTCGGCGGCTCGTGGCTCTTTCGCGGCAAAAAGGATTTG
-----E2f-1 PROMOTER-----
481 GCGCGTAAAAGTGGCCGGGACTTTGCAGGCAGCGGCGGGGGCGGAGCGGGATCGAG
-----E2f-1 PROMOTER-----
541 CCCTCGATGATATCAGATCATCGGATCCCGGTCGACTGAAAATGAGACATATTATCTGCC
-----+ +-----
601 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
-----E1a GENE-----
661 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT
-----E1a GENE-----
721 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
-----E1a GENE-----
781 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
-----E1a GENE-----
841 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCT
-----E1a GENE-----

Fig. 3A



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901 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGG
-----E1a GENE-----

961 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
-----E1a GENE-----

1021 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCAATTATCACCGGAGGAATACGGGGGACC
-----E1a GENE-----

1081 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
-----E1a GENE-----

1141 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTTTTTTAAT
-----E1a GENE-----

1201 TTTTACAGTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGTC
-----E1a GENE-----

1261 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCTCTAA
-----E1a GENE-----

1321 AATGGCGCCTGCTATCCTGAGACGCCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
-----E1a GENE-----

1381 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC
-----E1a GENE-----

1441 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG
-----E1a GENE-----

1501 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG
-----E1a GENE-----

1561 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTGCTGAATGAGT
-----E1a GENE-----

1621 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC
-----+-----

1681 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA
-----E1b GENE-----

1741 GGCTTGGGAGTGTTTGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA
-----E1b GENE-----

1801 CA
--

Fig. 3B



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33881 AACCTACGCCCAGAAACGAAAGCCAAAAACCCACAACCTCCTCAAATCGTCACTTCCGT
33941 TTTCCCACGTTACGTCACTTCCCATTTTTAATTAAGAATTCTACAATTCCCAACACATACA
34001 AGTTACTCCGCCCTAAAACCCTGGGCGAGTCTCCACGTAAACGGTCAAAGTCCCCGCGGC
+-- PACKAGING SIGNAL-----
34061 CCTAGACAAATATTACGCGCTATGAGTAACACAAAATTATTCAGATTTCACTTCCTCTTA
-----PACKAGING SIGNAL-----
34121 TTCAGTTTTCCCGCGAAAATGGCCAAATCTTACTCGGTTACGCCCAAATTTACTACAACA
-----PACKAGING SIGNAL-----
34181 TCCGCCTAAAACCGCGCGAAAATTGTCACTTCCTGTGTACACCGGCGCACACCAAAAACG
-----+
34241 TCACTTTTGCCACATCCGTCGCTTACATGTGTTCCGCCACACTTGCAACATCACACTTCC
34301 GCCACACTACTACGTCACCCGCCCCGTTCCCACGCCCCGCGCCACGTCACAAACTCCACC
+-----ITR-----
34361 CCCTCATTATCATATTGGCTTCAATCCAAAATAAGGTATATTATTGATGATG
-----ITR-----+

Fig. 3C



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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
----- ITR -----
61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGCCGCTAGCGAT
----- ITR ----- ++ --- MCS -----
121 ATCGGATCCCGGTGCGACTGAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGA
----- E1a -----
181 AGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCC
----- E1a -----
241 ACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGC
----- E1a -----
301 CCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGC
----- E1a -----
361 GGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCC
----- E1a -----
421 TCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCC
----- E1a -----
481 AAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGA
----- E1a -----
541 CGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGG
----- E1a -----
601 TTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCT
----- E1a -----

Fig. 4



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```
1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----
61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
-----ITR-----+ +-----
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----
181 ACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATATCGGATCCCGGTGCGACT
-----+ +-----
301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCT
-----E1a-----
361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGA
-----E1a-----
421 ACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGA
-----E1a-----
481 GGAGGCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGA
-----E1a-----
541 CTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCC
-----E1a-----
601 CGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGT
-----E1a-----
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Fig. 5



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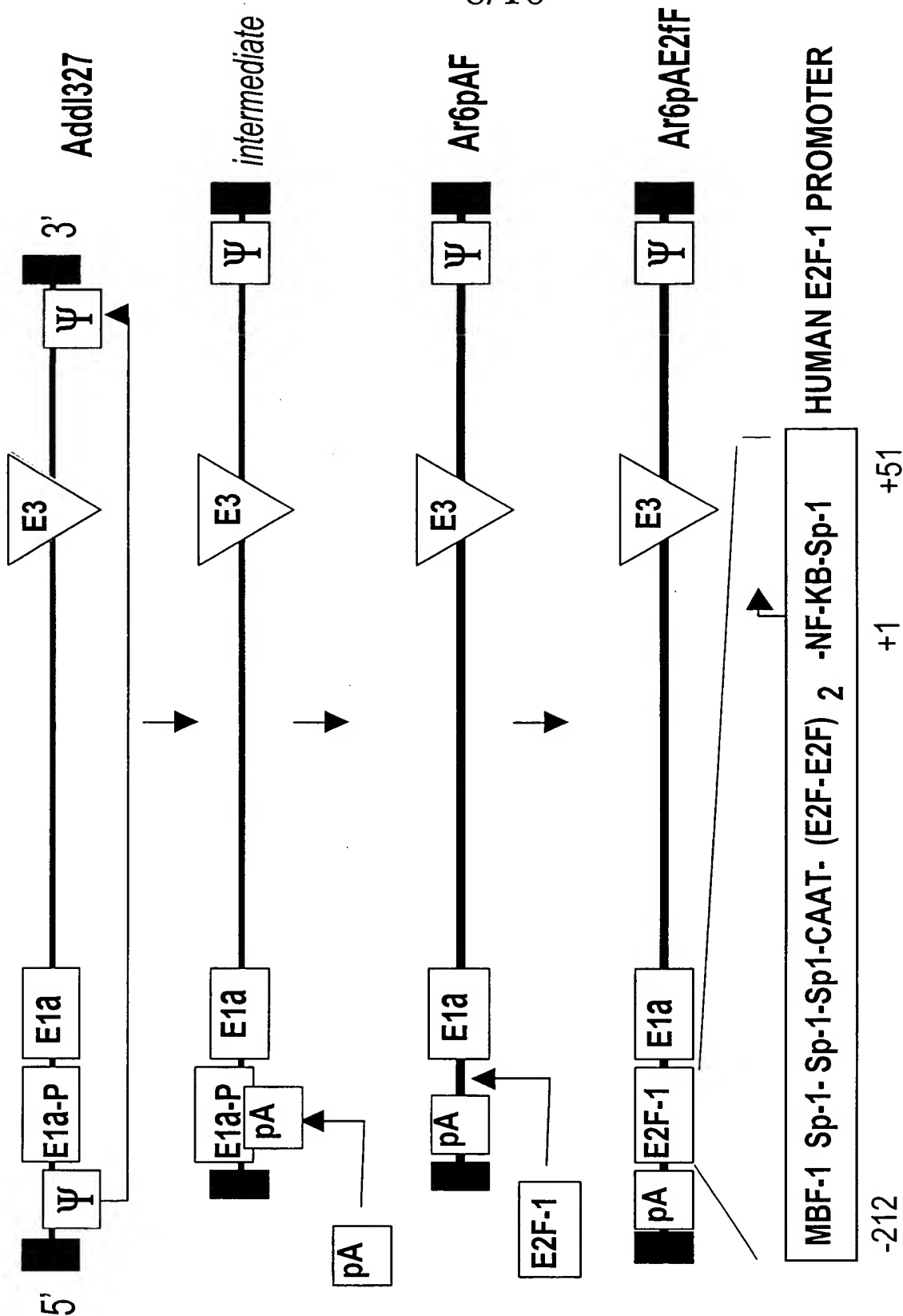


Fig. 6



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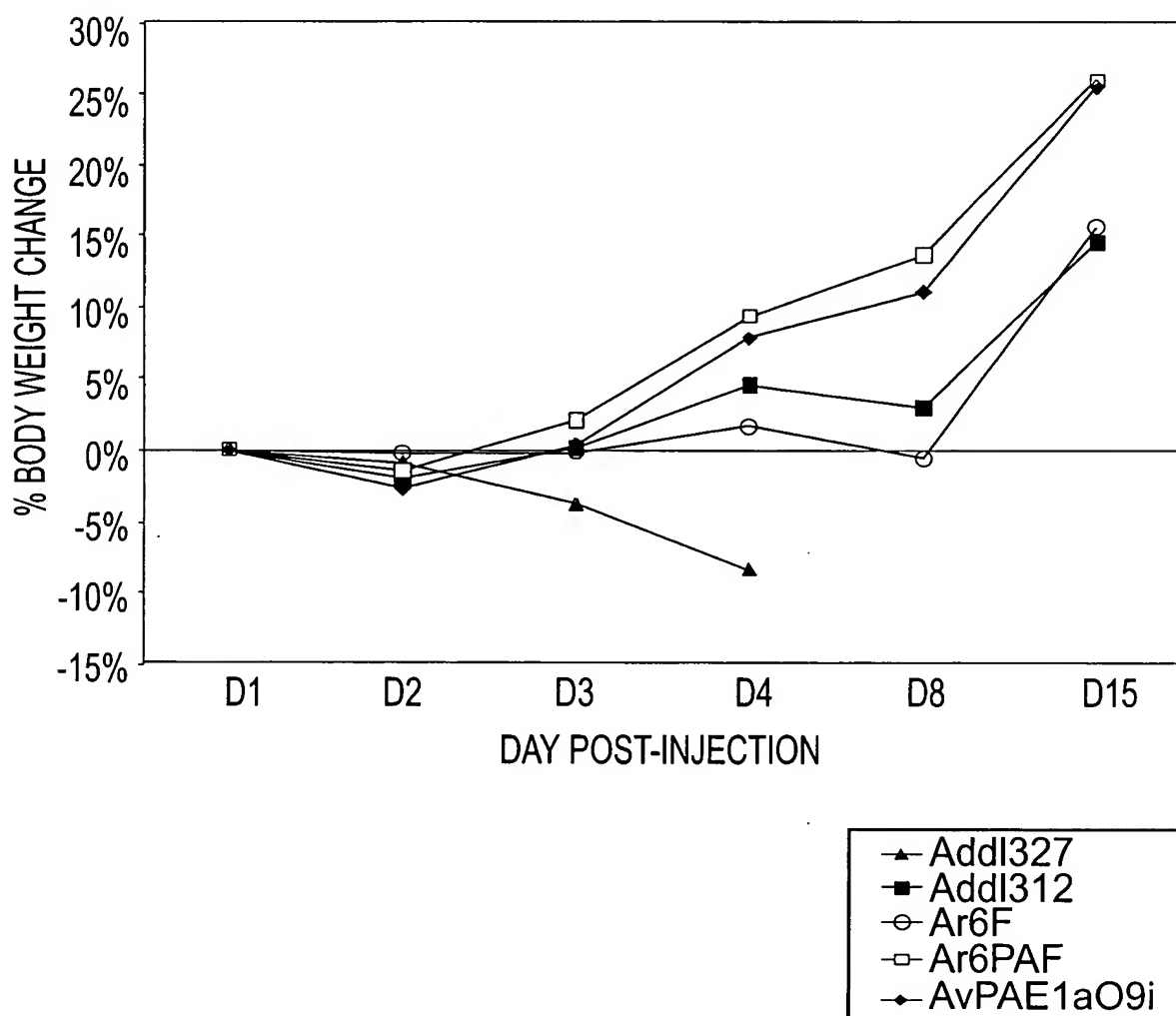


Fig. 7



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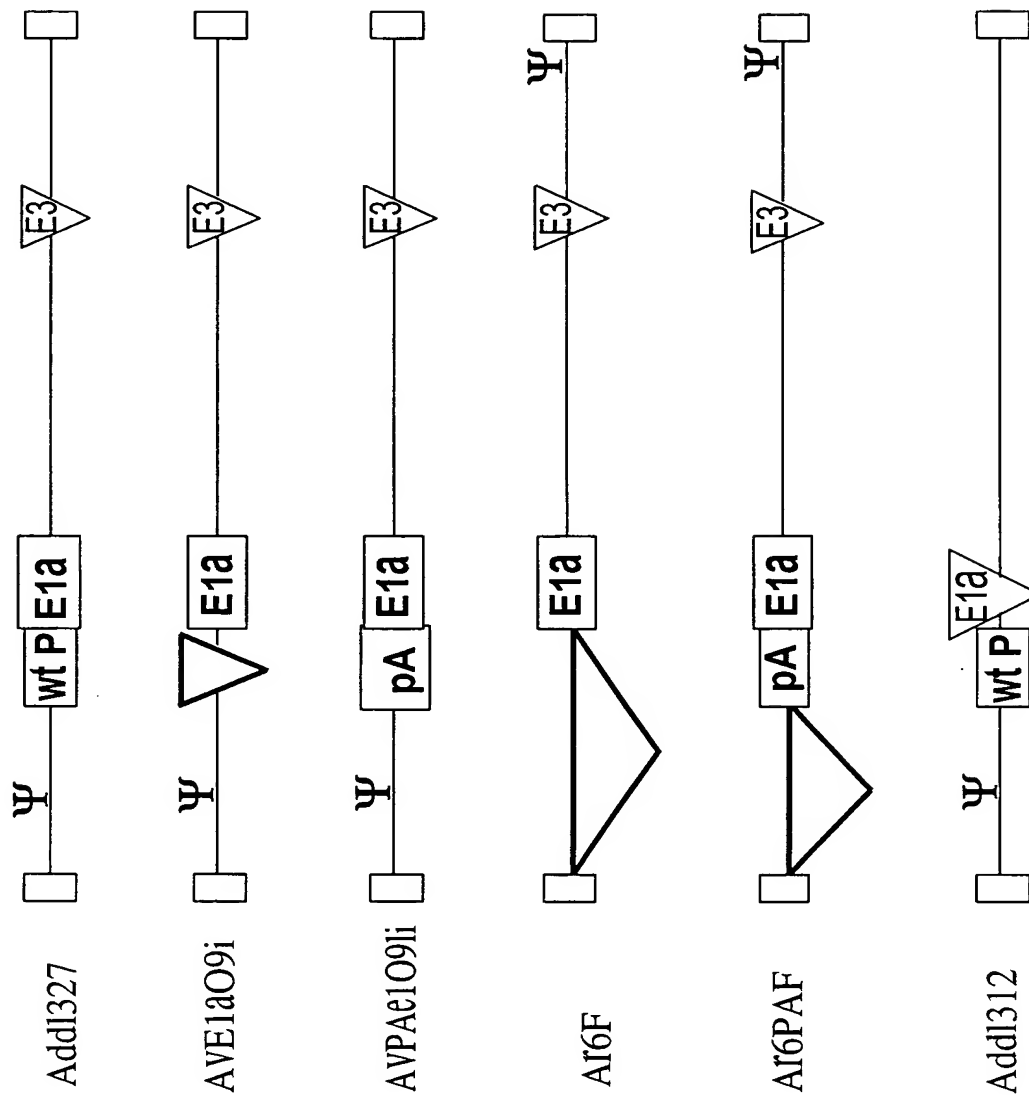


Fig. 8